

Minimum Number of Genes Controlling Cotton Fiber Strength in a Backcross Population

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ABSTRACT

Textile mills in the USA require strong cotton fiber (*Gossypium hirsutum* L.) for modern high-speed textile operations. The primary objective of this study was to determine the inheritance of strength descending from FTA 263-20 (FTA). FTA was developed by introgression into *G. hirsutum* from *G. arboreum* L., *G. thurberii* Todaro, and *G. barbadense* L. Five backcrosses (BCs) into 'Deltapine 16' (DP 16) followed by six BCs into DP 90ne were made. In 2001, three sets of 64 BC₆ F₂F₃ progenies were evaluated for strength. Significant variability for F₂F₃ strength ($F = 2.79$), yield, three yield components, and four other fiber traits were detected. From a three replication test, strength gene number(s) estimates ranged from 1.10 to 1.29 and combined over sets was 1.23 genes. Average strength for the three BC₅ parents was 10.3% greater than DP 90ne and yield was 16.9% less. Strength was highly correlated with lint percentage, boll weight, seed weight, and 2.5% span length. Gene numbers for these correlated traits ranged from 0.02 for micronaire to 1.04 for yield. A separate study involving the BC₅ parents, 'Deltapine 90' (DP 90) and DP 90ne was used to determine the major physical components of strength. Fineness and individual fiber strength had no effect. Short fiber content significantly impacted strength as the three BC₅ parents average short fiber was 6.7 versus 8.7% for the DP 90s. The BC₅ parents average strength was 11% higher, 240 vs. 219 kN m kg⁻¹, and its yield was 9.0% lower than DP 90ne. Probably a single major gene or closely linked cluster of genes resulted in increased fiber strength.

THE U.S. COTTON AND TEXTILE industry has been described as an industry in crisis. Labor, regulatory controls, and technology costs are less in competing countries than in the USA. As a result, many U.S. textile operations closed or moved to other countries. As a result, U.S. grown cotton used by the U.S. textile industry has also decreased from about 11 million bales for the 1996 to 1997 and 1997 to 1998 periods to the current estimate of 7.4 million bales (USDA, Foreign Agricultural Service, 2003). The remaining U.S. textile industry is modernizing by shifting to high-speed ring, open end, and air jet spinning (Felker, 2001). Machines that in 1988 required 15.5 min to weave have been replaced with air jet looms that require less than 2.5 min to weave the same fabric (Felker, 2001). The new machinery requires higher fiber quality, including fiber strength, than is currently being used for maximizing both efficiency and product quality. The USDA-AMS (2003) reports fiber strength has not been increasing for the last 10 yr. The most efficient way to increase fiber strength is through genetics and breeding. The genetic, environmental, and genetic \times environmental variance components are 43.5,

34.3, and 22.2%, respectively of the total variance components as indicated in the analysis of 36 yr of high quality cultivar testing (Meredith, 2003). The lack of breeding progress for fiber quality has led some (Felker, 2001) to question if modern U.S. cotton breeders were mindful of their best customers' fiber needs.

Fiber bundle strength (T_1) has long been recognized as being inherited as a quantitative trait (Richmond, 1951). It is generally assumed that high fiber strength is caused by many genes. Self and Henderson (1954) in populations involving high strength AHA 50 and 'Half and Half' reported Pressley strength was determined by five genes. Tipton et al. (1964) with F₂ plant populations of 'Cleveland Short Sympodia' \times AHA-6-1-4 and Cleveland Short Sympodia \times 'Stardel' estimated the number of genes to be 12 to 13 and 13 to 14, respectively. Both studies used the Castle-Wright formula for estimating number of genes.

May (1999) concluded in his review that fiber strength was quantitatively inherited. Recent genomic studies reinforce that many genes are involved in fiber strength inheritance. Shapley et al. (1998) using RFLP molecular markers, identified six linkage groups associated with fiber strength inheritance. Ulloa and Meredith (2000) detected three QTLs associated with fiber strength. In a large *G. hirsutum* \times *G. barbadense* population, Patterson et al. (2003) recorded 21 QTLs while Zhang et al. (2003) detected nine molecular markers linked to two QTLs for fiber strength. One QTL in their study accounted for 18.5 to 53.8% of the total phenotypic variance and they considered this QTL a major gene for fiber strength. In Ulloa and Meredith's (2000) study, one QTL explained 24.6% of the strength variation and a second explained 10.6%. After a BC study to improve fiber strength, Meredith (1977) suggested that a relatively small number of major genes are conditioning fiber strength, perhaps as few as one or two in the genotypes utilized. Meredith (1992) continued the backcross program but changed to another recurrent parent, 'DPL90ne'. In BC₂, he recorded four high strength lines from a small population of nectariless (ne_1 , ne_2) progeny that averaged 9% higher strength than its recurrent parent. One of these lines was released as a cultivar 'MD51ne' (Meredith, 1993).

Some of the components of T_1 are fiber length and its distribution, fineness, and individual fiber strength. A previous study using a sample of 24 *G. hirsutum* cultivars (Meredith, 1992) reported that the fiber trait most influencing T_1 was 50% span length which accounted for 22% of the total variation. The interaction of 50% span length, fineness, and individual fiber strength accounted for another 23.8%. The major objective of this study was

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Abbreviations: AFIS, Automated Fiber Information System; BC, backcross; DP, Deltapine; FTA, FTA 263-20; HVI, high volume instrumentation; QTL, quantitative trait loci; T_1 , fiber bundle strength.

to use advanced backcross populations (BC_6) to estimate the number of genes conditioning fiber strength in a DP 90 background. The only trait selected in these BCs was T_1 . A second objective was to measure the change in yield, yield components, and other fiber traits that occurred during this backcross procedure. A final objective was to evaluate other components of T_1 that were contributing to higher strength.

MATERIALS AND METHODS

Backcross programs were used to develop populations in which to estimate the minimum number of genes determining fiber strength. The study reported herein was a continuation of a backcross program (Meredith, 1977) designed to introduce high strength genes from FTA into Midsouth type cottons. FTA is a single plant selection from the germplasm release FTA, GP 154 (Culp and Harrel, 1980). The high strength originated from the tri-species hybrid, (*G. arboreum* \times *G. thurberi*) \times *G. hirsutum*, crossed and intercrossed with *G. barbadense* and *G. hirsutum*. A total of 11 backcrosses were made since the original cross of DP 16 \times FTA. Five backcrosses were made into the DP 16 background followed by six more into the DP 90 background. DP 16 accounts for 50% of the parentage of DP 90 (Calhoun et al., 1997). Following the initial three backcrosses to a nectariless isolate of DP 16, (Meredith, 1977) two additional backcrosses were made to DP 16ne with selection for high strength and the nectariless trait. After BC_2 , DP 90ne, the progenies whose strength exceeded the recurrent parent by 10%, were grown in replicated tests and again evaluated for strength. The single progeny that was most consistent in producing high strength was used to initiate the next generation. A strain of the BC_5 , designated as MD 65-11ne was used to initiate the second backcross program into DP 90. Half of the parentage of DP 90 was DP 16 (Calhoun et al., 1997). The F_1 of MD 65-11ne \times DP 90 was produced in 1984 followed by a backcross to DP 90 in a winter increase nursery in Mexico. The BC_2 was made from the $BC_1 F_1 \times DP 90$. Four $BC_2 F_{2.3}$ progenies had 10% greater strength than DP 90. All subsequent BCs were made to DP 90ne. Three $BC_5 F_{2.4}$ progenies,

Table 1. Backcross (BC) history used to develop the BC_5 and BC_6 populations.

Year of cross	Parents†	Seed produced	Years of BC $F_{2.3}$ progeny tests	Total no. of progenies‡
1984	DP 90 \times MD 65-11ne	$BC_1 F_1$	—	—
1985	$BC_1 F_1 \times DP 90ne$	$BC_2 F_1$	1987	60
1988	$BC_2 \times DP 90ne$	$BC_3 F_1$	1990	136
1993	$BC_3 \times DP 90ne$	$BC_4 F_1$	1994	160 (2)
1996	$BC_4 \times DP 90ne$	$BC_5 F_1$	1997	32
2000	$BC_5 \times DP 90ne$	$BC_6 F_1$	2001	192 (3)

† DP 90, 'Deltapine 90'.

‡ Number of sets used to produce the total number of progenies are indicated in parentheses.

BC_5 -12, BC_5 -32, and BC_5 -36, were used as parents and each produced a set of 64 progenies. The BC procedure used to produce the BC populations is listed in Table 1.

A genetic set consisted of 64 $BC_6 F_{2.3}$ progenies, and their BC_5 and DP 90ne parents. The progenies were grown in plots, 6.5 by 1.0 m, and were replicated three times. Two entries of each parent were grown in each set. The three sets were randomized within each replication. Plots were planted 25 April 2001. Cultural and pest control methods were standard for the production area. Yield components were determined from 50 boll samples, taken just before hand harvest. Lint percentage is the mass of lint ginned from the sample of seed cotton, expressed as a percentage, boll weight is seed cotton weight (in grams) per number of bolls in a sample, and seed weight is the average weight of 100 fuzzy seeds, expressed as milligrams per seed. Fiber traits given in Table 2 were determined by Starlab, Inc., Knoxville, TN. Strength is determined by the stelometer and measures the force per tex required to break a bundle of fibers (expressed as kilonewton meter per kilogram). These bundles of fibers are held by two jaws separated by 3.2 mm. Elongation is the percentage of elongation at the point of break in strength determination. Micronaire is an indicator of fiber fineness and/or fiber maturity and was measured by the Fibronaire instrument and is expressed in micronaire units. The 50 and 2.5% span lengths are measured on the Digital Fibrograph, and they are the average length of the longest 50 and 2.5%, respectively, of the fibers scanned.

Table 2. Average lint yield, yield components, and fiber properties from genetic study for three sets of $BC_6 F_{2.3}$ progenies, and the $BC_5 F_{2.5}$ and Deltapine 90ne (DP 90ne) parents†.

Genetic population	Lint yield kg ha ⁻¹	Lint %	Boll weight g	Seed weight mg	Strength (T_1) kN m kg ⁻¹	Elongation %	Micronaire	Span length	
								50% mm	2.5% mm
Set 12									
DP 90ne	964**	38.1**	4.01	7.9	224	6.4	44.3	13.9	28.2
$BC_5 F_{2.5}$	767	36.2	4.05*	8.7**	244**	6.0	43.0	14.4**	29.2**
$BC_6 F_{2.3}$	855	37.5	4.09	8.2	240	6.2	44.3	14.1	28.5
Set 32									
DP 90ne	883**	37.8**	4.13	8.0	226	7.8**	44.2	14.1	28.0
$BC_5 F_{2.5}$	687	36.2	4.18*	8.6*	248**	6.2	45.8**	13.9	28.0
$BC_6 F_{2.3}$	835	38.1	3.93	7.9	229	6.9	43.5	13.9	28.1
Set 36									
DP 90ne	875	38.6**	4.03	8.1	223	6.4*	47.0**	13.9	27.9
$BC_5 F_{2.5}$	812	37.1	4.22**	8.7*	248**	5.8	43.3	14.2	29.0**
$BC_6 F_{2.3}$	852	36.7	4.01	8.6	240	6.6	44.1	14.3	28.7
Combined									
DP 90ne	907**	38.1**	4.06	8.0	224	6.9**	45.2**	14.0	28.1
$BC_5 F_{2.5}$	755	36.5	4.15**	8.7**	247**	6.0	44.1	14.2*	28.7**
$BC_6 F_{2.3}$	848	37.4	4.01	8.2	236	6.6*	44.0	14.1	28.5
Midparent	831	37.3	4.10	8.4*	236	6.4	44.6*	14.1	28.4
t (0.01)‡	82	0.6	0.02	0.3	6	0.3	0.2	0.1	0.2
F test	1.45**	2.68**	1.53**	2.54**	2.71**	2.04**	2.38**	1.44**	1.58**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

† t test comparisons between the two parents were made for each set and for the combined means. F test given for variation among BC_6 progenies.

‡ t test value at 0.01 probability level to compare $BC_6 F_{2.3}$ with DP 90ne and $BC_5 F_{2.5}$.

Lint yield is determined as harvested seed cotton weight including 50 boll sample \times lint fraction.

Yield, yield components, and fiber properties for the three BC₅ parents and DP 90ne and DP 90 were determined similarly to the above progeny rows. The exception being the tests were conducted at two locations near Stoneville, MS. Planting dates were 20 and 27 April 2001. Yield was determined from six replications at each site. Yield components were obtained by combining 50 boll samples taken from two adjacent replications. Lint from the combined replications were used to determine the fiber properties. In addition, fibers were analyzed by the Automated Fiber Information System (AFIS). Mean short fiber content measures the percentage by weight of the fibers that are less than 12.7 mm. The mean length by weight is determined by AFIS. Fiber fineness measures the weight of fibers per unit of length in millitex. Maturity ratio is a measure of the proportion of mature fibers divided by the immature fibers. The MANTIS instrument was used to estimate fiber strength from 500 individual fibers from each of three replications of BC₅-32 and DP 90ne. The tests were conducted at Cotton Incorporated, Cary, NC.

Minimum number of genes was estimated by the Castle-Wright formula (Wright, 1968) as modified by Cockerham (1986). Standard error estimates of number of genes were taken by the method proposed by Lande (1981).

RESULTS AND DISCUSSION

The means for fiber strength and eight other traits for DP 90ne, the BC₅ parents, and their BC₆ population for each set are given in Table 2. The mean over all sets and the *F* values for progenies are given plus the *t* value for comparing BC₆ F₂₃ with DP 90ne and BC₅ F₂₅. The *F* values for the 192 progenies are significant at the <0.001 probability level for all traits. After 11 backcrosses significant genetic variability still exists for all other traits. This implies that the genetics of strength also influenced the other traits. One type of mean comparison in Table 2 involves comparison of the recurrent parent, DP 90ne, and specific BC₅ parents. The BC₅ parents averaged 23 kN m kg⁻¹ or 10.3% higher strength than DP 90ne. The difference in the BC₃ original study (Meredith, 1977) was 23 kN m kg⁻¹. A high level of strength expression maintained in the backcross selection practice is evident. Meredith (1977) speculated that the negative association between yield and strength might be reduced with further backcrossing, as some of the negativity might be due to linkage. However, the average yield difference in this study between recurrent parent and BC₃ selections was 124 kg ha⁻¹ or 11.5% in the first study (Meredith, 1977) and the average yield

difference of BC₅ parents vs. DP 90ne is 152 kg ha⁻¹ or 16.8%. This suggests that the negative association of traits with strength is not due to linkage, but due to pleiotropic gene action. Part of the decreased yield (4.2%) is due to a significantly lower lint percentage for the BC₅ parents than that for DP 90ne. The recurrent parent also had higher elongation and micronaire, smaller boll and seed weight, and shorter 50 and 2.5% span length.

The phenotypic correlations among traits from the 192 BC₆ progenies are given in Table 3. Twenty-four of the 36 traits were correlated at the 0.01 probability level, but the correlations were small. This was probably influenced by the small number (three) of replications per progeny. The strongest correlations with strength were lint percentage, $r = -0.33$; seed weight, $r = 0.39$; elongation, $r = -0.37$; 50% span length, $r = 0.48$; and 2.5% span length $r = 0.49$. No significant correlations of strength and yield ($r = 0.04$) and micronaire ($r = -0.04$) were detected in the BC₆ progenies. However, the comparison of three BC₅ parents mean strength vs. DP 90ne was significant in both the progeny and components of strength tests (Tables 2 and 4).

The comparison of midparent vs. BC₆ means in Table 2 was made to test for nonadditivity. The average strength for both midparent and BC₆ was 236 kN m kg⁻¹. Only three traits showed significance for nonadditivity. These were seed weight, elongation, and micronaire, whose deviations from midparent average were 2.4, 3.0, and 1.3%, respectively.

Estimating the Minimum Number of Genes

The estimated maximum number of genes for strength and eight other traits is given in Table 5. The estimates of gene number for strength was similar in all three sets. The estimates are 1.10, 1.29, and 1.23 for sets 12, 32, and 36, respectively. The standard error of estimates also are similar; about 0.34. The combined estimate is 1.23 genes with a standard error of 0.16. Also, the high level of recovery of strength for 11 backcross generations using small populations, implies a small number of genes or linkage groups is involved in the inheritance of strength for this study. Zhang et al. (2003), using molecular markers identified a QTL_{FSI} for strength which descended from Acala B3080, that explained 18.5 to 53.8% of the total phenotypic variance for strength. Acala B3080 further has a pedigree that shows interspecific contribution. Zeng et al. (1990) indicated that it would be difficult to separate the estimates of single

Table 3. Correlations† of traits involving 192 BC₆ F₂₃ progenies derived from crossing BC₅ F₂₄ bundle strength selections with its recurrent parent, Deltapine 90ne (DP 90ne).

Trait	Lint %	Boll weight	Seed weight	Strength (T ₁)	Elongation	Micronaire	Span length	
							50%	2.5%
Yield	0.37	0.24	0.01	0.04	0.06	0.02	0.11	0.04
Lint %		-0.12	-0.52	-0.33	0.16	-0.04	-0.31	-0.33
Boll weight			0.59	0.25	-0.18	0.31	0.24	0.31
Seed weight				0.39	-0.24	0.29	0.53	0.53
Strength (T ₁)					-0.37	-0.04	0.48	0.49
Elongation						-0.23	-0.10	-0.20
Micronaire							-0.02	-0.26
50% span length								0.73

† Significantly greater than zero, if $r > 0.14$, 0.18, and 0.24 at the 0.05, 0.01, and 0.001 probability levels, respectively.

Table 4. Average yield, yield components, and fiber properties from two locations for Deltapine 90 (DP 90), Deltapine 90ne (DP 90ne), and three BC₅ F₂₅ parents used to produce the BC₆ F₂₃ genetic populations.

Parental type	Lint yield		Boll weight	Seed weight	Lint weight	Seed boll	Fiber properties				Maturity ratio	Span length			Short fiber
							Strength (T ₁)	Elongation	Micronaire	Fineness		50%	2.5%	Mean	
	kg ha ⁻¹	%	g	mg	No.			%		mtex		mm			%
DP 90	868	38.6	4.31	8.9	5.6	29.6	219	6.0	48.0	173	93.0	14.0	28.6	24.0	8.7
DP 90ne	781	39.4	4.36	9.4	6.1	29.0	219	6.2	46.8	171	93.7	14.2	28.8	24.0	8.7
BC ₅ -12	739	36.9	4.41	9.7	5.7	28.7	238	5.8	47.0	175	95.2	14.9	30.0	25.8	7.2
BC ₅ -32	699	36.0	4.43	9.5	5.4	29.7	242	6.1	46.3	174	95.2	14.5	29.5	25.4	6.5
BC ₅ -36	672	37.1	4.53	10.0	6.0	28.6	239	5.5	47.7	179	96.0	14.6	29.4	25.8	6.5
LSD 0.05	110	0.9	0.18	0.3	0.3	1.2	8	0.6	3.1	4	1.3	0.9	0.9	0.6	0.4
DP average	824**	39.0**	4.33	9.1	5.9**	29.3	219	6.1	47.4	172	93.3	14.1	28.7	24.0	8.7**
BC ₅ average	703	36.7	4.46*	9.7**	5.7	29.0	240**	5.8	47.0	176**	95.4**	14.7	29.6**	25.7**	6.7

* *t*-test comparisons for Deltapine average vs. BC₅ average significant at the 0.05 probability level.

** *t*-test comparisons for Deltapine average vs. BC₅ average significant at the 0.01 probability level.

genes from linkage blocks which contained several genes influencing the same trait. In these studies, the number of genes or linkage groups conferring fiber strength was small, probably one or two. Expanded use of cotton genomics should solve this question.

The selection for high fiber strength affected other traits. If the gene or genes conferring fiber strength also caused the genetic variability for these traits, then their estimated gene number should mimic that of strength. The estimates of gene number in Table 5 for these traits ranges from 0.02 for micronaire to 1.04 for lint yield. Lint percentage with an estimate of 0.59 had the highest estimate of the yield components. Elongation percentage and 2.5% span length, components of T₁, had estimates of 0.87 and 0.60, respectively. The estimates do not perfectly mimic that of fiber strength. However, the estimate of a small number of genes for the correlated traits is in keeping with the conclusion that a small number of genes is having major effects on fiber strength and its correlated traits.

To many geneticists, quantitatively inherited traits imply a large number of genes each with small effects. Therefore, the methods of accurately estimating the number of genes generally are difficult and not pursued. Zeng et al. (1990) in their evaluations on estimation of gene number stated, "we are still painfully short of a reliable method to do it." As a result, most breeding is conducted as if all quantitative traits are determined by many genes, each with small effects. The Castle-Wright procedure and its modification by Cockerham (1986) has been used sparingly, because the four basic assumptions for its use rarely describe a real population. These four basic assumptions are (i) all plus (+) effects enter into the segregating population from one parent and all minus (−) effects enter from the other parent, (ii) no dominance or nonadditive gene action, (iii) all

genes have equal effects, and (iv) no linkage. If these assumptions are not met, the true number of genes determining a trait is underestimated. In this study, the first two assumptions appear not to be major problems. Repeated strong selection for strength in each backcross population eventually insures that all the plus effects come from the selected donor parent. The comparison of midparent vs. BC₆ average strength shows strength to be 236 kN m kg⁻¹ for both groups. This comparison for the other traits shows statistical significance ($P < 0.05$) for three traits; seed weight, elongation, and micronaire. These three comparisons deviate 2.4, 3.0, and 1.3%, respectively from the midparent mean. As the true number of genes increases, the likelihood of equal effects for all genes decreases causing estimation problems to increase. The assumption of no linkage is more complicated. FTA, the source for high strength in this study, has major introgression from three exotic species (Culp and Harrel, 1980). Exotic DNA segments could have low homology with *G. hirsutum* DNA, potentially resulting in large linkage groups with essentially no recombination. Thus, Zeng et al. (1990) suggested that the estimate of gene number would essentially be the number of chromosomes that impact a specific trait.

Components of Fiber Bundle Strength

A second objective was to investigate basic fiber traits that are components of strength. The common physical fiber properties thought to be components of strength are length of the fiber, fineness, and individual fiber strength. The AFIS instrument was used to measure the first two factors and the MANTIS at Cotton Incorporated was used to measure individual fiber strength. These studies were performed using fiber from an additional study comparing DP 90, DP 90ne, and the three

Table 5. Estimated minimum number of genes† for fiber traits.

Parental BC ₆ set	Fiber traits				Yield and yield components				
	Strength (T ₁)	Elongation (E ₁)	Span length		Micronaire	Lint yield	Lint %	Boll weight	Seed weight
			50%	2.5%					
12	1.10 (0.34)	1.44 (1.48)	0.80 (1.95)	8.28 (207)	0.14 (0.03)	0.51 (0.24)	0.78 (0.20)	−0.14 (70.5)	0.48 (0.17)
32	1.29 (0.35)	10.83 (48.4)	−0.93 (32.6)	−0.98 (921)	−0.05 (0.03)	3.30 (10.5)	1.28 (0.60)	−1.11 (19.4)	0.39 (0.14)
36	1.23 (0.34)	0.51 (0.12)	−0.12 (0.09)	0.44 (0.19)	0.11 (0.03)	0.36 (0.27)	0.15 (0.02)	−0.16 (0.19)	0.59 (0.21)
Combined	1.23 (0.16)	0.87 (0.25)	−0.08 (0.03)	0.60 (0.32)	0.02 (0.00)	1.04 (0.47)	0.59 (0.07)	−0.09 (0.09)	0.53 (0.10)

† Standard error given in parenthesis.

BC₅ lines used to make the BC₆ populations noted above. The means from two locations for yield and its components, strength, and AFIS fiber properties are given in Table 4. The yield and yield components means are very similar to those given in Table 2. Fiber strength of the BC₅ averaged 11% higher than the DP cultivars. Highly significant differences for all fiber traits except micronaire and elongation were detected. Fineness can confer greater T₁ as more fine fibers can be placed in a bundle of a given weight of fiber than that for coarser fibers with the same weight. It is evident that fineness is not resulting in greater T₁ as the BC₅ parents' fineness is coarser than that of the DP cultivars. The maturity of the BC₅ lines also was greater than that of the DP cultivars. The largest differences between the DP cultivars and BC₅ lines was with length, especially short fiber content. Short fiber content is the amount, by weight, of fibers that are less than 12.7 mm in length. The reduction from 8.7 to 6.7% for a 26.4% reduction is unusual, especially since selection was not practiced for this trait. Apparently, the combination of increased length of all length measurements and short fiber content had a great impact on fiber T₁. A reduction in short fiber is also of major significance as short fibers are wasted at the textile mill and also result in reduced spinning efficiency and yarn quality. The third factor thought to influence a bundle of fibers is the average fiber strength of the individual fibers. Individual fiber strength from lint samples for three replications of DP 90ne and BC₅-32 was made by Cotton Incorporated. The strength to break for DP 90ne and BC₅-32 averaged 5.89 and 5.85 kN m kg⁻¹, respectively, and their respective elongations were 14.3 and 13.7%, respectively. These results indicate that perimeter and individual fiber strength were not major contributors to the increased fiber strength, and that short fiber content had the major impact on fiber strength.

Cotton Breeding Implications

There are three areas that a small number of genes and its association with other traits can impact breeding efficiency. First, the backcross breeding method and its simplicity in use can be demonstrated by this study and the earlier studies (Meredith, 1977). Second, fewer resources are required for a small number of genes controlling a trait as compared with many genes. For example, the number of F₂ progenies needed to have a 95% chance of finding at least one progeny that has the desired genotype is 11 if the trait is controlled by one gene, 47 if controlled by two genes, and 3.14 million if the trait is controlled by 10 genes. Due to estimates of 1.23 genes in this study and the consistency in recovering an increase in fiber strength of about 10% from small populations, support the conclusion that in this population, strength is conferred by one gene or one closely linked block of genes. Since no current U.S. cotton breeder has segregating populations numbering in the millions, it is likely that selection for major genes occur more often than is commonly assumed. As noted above, genomics has identified several QTLs that have

major effects on fiber strength. Several studies note the epistatic interactions that are taking place between the A and D genomes. Diploids having A genome lint generally have short, weak, and coarse fiber, while the diploid D genome has no spinable fibers. However, the allotetraploid species *G. hirsutum* and *G. barbadense* have longer, stronger, and finer fibers than that of the diploid genomes. Jiang et al. (1998) reported that the merger of the A and D genomes offered unique opportunities for improvement for many traits, including fiber quality. Jiang et al. (2000) reported a preponderance of interspecific allelic interactions involving one locus from the A genome and the other from the D genome.

The third factor involving selection of major genes is the undesirable association of traits, for example, strength and yield. The cause of genetic associations is either linkage or pleiotropy. If linkage is the case, as with many crosses involving *G. hirsutum* with exotic material, the backcross procedure will greatly aid in reducing the undesirable genes. In this study, linkage is not the case. In this study, a total of 11 backcrosses from FTA has occurred, thus it is unlikely that the observed changes in yield and lint percentage are due to linkage. The associated fiber traits involving fiber length distributions is explainable as they are components of fiber strength. The negative association of yield and fiber strength has continued even after many generations of backcrossing. Culp et al. (1979) reported their success in reducing the negative association was to regularly cross the best yield-strength combinations from one introgressed population with other introgressed populations. They reported that this method reduced the negative yield association from -0.93 to 0.16. This change was associated with an increase in the number of harvestable bolls.

They attributed the change to the breakup of linkage blocks, but the change could also have been due to selecting for compatible interactions from different genetic backgrounds. Meredith (2003) reported that the relationship of yield and strength was still negative after 36 yr of selection but that the negative relationship had been reduced. This study involved evaluating the changes that occurred in the National Regional High Quality Study. Different genetic backgrounds can have different genetic associations with yield. Selection within these populations can reduce the negative strength-yield association. The BC₂-derived MD 51ne cultivar's yield equaled that of DP 90 and its strength was 10% higher (Meredith, 1993). Genetic background effects also have been detected among transgenic cultivars for their expression of the *Bacillus thuringiensis* Berliner (Bt) *Cry1Ac* gene. Cultivars descending from 'DP 5415' showed a 305% higher Bt endotoxin level than from other cultivars (Adamczyk and Meredith, 2003). The average mean Cry1Ac was 8.5 mg kg⁻¹ for DP 5415 background and 2.8 mg kg⁻¹ for 'ST 474' and 'PM 1200' backgrounds. The genetic analysis with two genetic populations showed that the high level of Cry1Ac was due to one major gene, which could be efficiently selected for in backcross populations (Adamczyk and Meredith, 2003). Thus far, no U.S. transgenic cultivars have been released commercially that were not developed by the BC method. This

study and several genomic studies suggest other major genes exist in which effective selection within small populations would be effective. This suggests a potential for finding genetic backgrounds that have lower yield–fiber quality negative associations than were encountered in this study.

This study offers germplasm that has been selected away from the high strength germplasm FTA by 11 backcrosses. Since most nonstrength genes from FTA are expected to have been lost due to the backcross selection procedure, these selected populations and their recurrent parent, DP 90ne, offer excellent genetic material for studying cotton physiology relations in yield and fiber strength.

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